

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2004, 20:15:24 ; Search time 61 Seconds
(without alignments)

736.902 Million cell updates/sec

Title: US-09-648-310-2

Perfect score: 406
Sequence: 1 MNVEHVNLLVEETHRLGSK.....AGELLQGVHDDVDIVLLQD 81

Scoring table:

	BLOSUM62
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlp
-Q=/cgm2_1/USPTO_spool_p/US09648310/runat_27082004_154406_27960/app_query.fasta_1.526
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -NATRX=blosome2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09648310 @CGN 1 1 141 @runat_27082004_154406_27960 -NCFU=6 -ICPU=3
-NO.WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgm2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgm2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgm2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgm2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgm2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	90.6	800	4	US-09-644-460-26
2	351	86.5	786	4	US-09-023-655-79
3	67	16.5	1449	4	US-09-252-991A-13298
4	67	16.5	2028	4	US-09-252-991A-12500
5	67	16.5	2040	4	US-09-252-991A-12977
6	66.5	16.4	393	4	US-09-252-991A-12137
7	65	16.0	421	4	US-09-313-294A-4253
8	65	16.0	1664976	4	US-08-916-421B-1
9	64	15.8	2133	4	US-09-328-352-1774
10	63.5	15.6	1134	4	US-09-252-991A-8104
11	63.5	15.6	1314	4	US-09-252-991A-8001
12	63.5	15.6	1755	4	US-09-252-991A-8133

c 13	63	15.5	1038	4	US-09-252-991A-13643	Sequence 13643, A
c 14	63	15.5	1266	4	US-09-252-991A-13795	Sequence 13795, A
c 15	62.5	15.4	2323	1	US-08-358-901-1	Sequence 1, Appli
c 16	62.5	15.4	2323	1	US-08-566-347-1	Sequence 1, Appli
c 17	62.5	15.4	2323	1	US-08-693-835-1	Sequence 1, Appli
c 18	62	15.3	2329	1	US-08-457-797A-8	Sequence 8, Appli
c 19	62	15.3	2329	1	US-08-812-025-8	Sequence 8, Appli
c 20	62	15.3	2329	3	US-09-138-873A-8	Sequence 8, Appli
c 21	62	15.3	28958	1	US-08-258-261B-6	Sequence 6, Appli
c 22	62	15.3	28958	1	US-08-456-837-6	Sequence 6, Appli
c 23	62	15.3	28958	1	US-08-457-343-6	Sequence 6, Appli
c 24	62	15.3	28958	1	US-08-457-646A-6	Sequence 6, Appli
c 25	62	15.3	28958	1	US-08-458-076A-6	Sequence 6, Appli
c 26	62	15.3	28958	1	US-08-764-233A-4	Sequence 4, Appli
c 27	62	15.3	28958	1	US-08-457-335A-6	Sequence 6, Appli
c 28	62	15.3	28958	1	US-08-729-214-6	Sequence 6, Appli
c 29	62	15.3	28958	3	US-09-028-934-6	Sequence 6, Appli
c 30	62	15.3	49377	1	US-08-764-233A-1	Sequence 1, Appli
c 31	61.5	15.1	669	4	US-09-252-991A-4849	Sequence 4849, Ap
c 32	61.5	15.1	1008	4	US-09-252-991A-4906	Sequence 4906, Ap
c 33	61	15.0	885	4	US-09-328-352-1423	Sequence 1423, Ap
c 34	61	15.0	885	4	US-09-489-039A-3762	Sequence 3762, Ap
c 35	61	15.0	1278	4	US-09-134-000C-2571	Sequence 2571, Ap
c 36	61	15.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 37	61	15.0	1830121	4	US-09-643-990A-1	Sequence 139, App
c 38	60	14.8	36800	4	US-08-311-731A-139	Sequence 1, Appli
c 39	60	14.8	640681	4	US-09-790-988-1	Sequence 6263, Ap
c 40	59.5	14.7	1419	4	US-09-252-991A-6269	Sequence 8717, Ap
c 41	59.5	14.7	1689	4	US-09-252-991A-8717	Sequence 6032, Ap
c 42	59.5	14.7	1965	4	US-09-252-991A-6032	Sequence 9230, Ap
c 43	59.5	14.7	1965	4	US-09-252-991A-9230	Sequence 188, App
c 44	59.5	14.7	2151	2	US-08-658-665-188	Sequence 41, Appl
c 45	59.5	14.7	2151	3	US-08-796-101-41	

ALIGNMENTS

RESULT 1
US-09-644-460-26
; Sequence 26, Application US/09644460
; Patent No. 6657053
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; TITLE OF INVENTION: Reciprocal Subtraction Differential
; TITLE OF INVENTION: Display
; FILE REFERENCE: 34587-C-PCT-USA
; CURRENT APPLICATION NUMBER: US/09/644,460
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US99/04323
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 09/197,889
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 09/185,115
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 09/032,684
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 800
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-644-460-26

Alignment Scores:
Pred. No.: 1.61e-48 Length: 800
Score: 368.00 Matches: 79
Percent Similarity: 95.18% Conservative: 0
Best Local Similarity: 95.18% Mismatches: 2
Query Match: 90.64% Indels: 2
DB: 4 Gaps: 0

US-09-648-310-2 (1-81) x US-09-644-460-26 (1-800)

```
QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 170 ATGAACGTGGACATGAGGTTAACTCTCTGGTGGAGGAATTCATCGTCTGGTTCCAAA 229
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
Db 230 AATGCCGATGGGAAACTCAGTGTGAAGTTTGGGGTCTCTTCCAGACGACAGATGTGCC 289
QY 41 AsnLeuPheGluAla-LeuValGlyThrLeuLysAla-AlaLysArgArgLysIleValT 60
Db 290 AATCTCTTTGAACCGTTGGTGGAACTCTGAAACCCCGCAACGAGGAGATTTGTTA 349
QY 60 hTyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeuG 80
Db 350 CGTAGCAGAGAGCTGCTTTTGAAGGTGTTTCATGATGATGTTGACATTTGATTGCTGC 409
QY 80 InAsp 81
Db 410 AAGAT 414

RESULT 2
US-09-023-655-79
; Sequence 79, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO. 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THP1PLB01
; CLONE: 012364
US-09-023-655-79

Alignment Scores:
Pred. No.: 7,48e-46 Length: 786
Score: 351.00 Matches: 75
```

```
Percent Similarity: 95.24% Conservative: 4
Best Local Similarity: 90.48% Mismatches: 1
Query Match: 86.45% Indels: 3
DB: Gaps: 0

US-09-648-310-2 (1-81) x US-09-023-655-79 (1-786)
QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 140 ATGAATGTGATCAGGAGGTTAACTCTTAGTGGAGGAATTCATCGTTTGGGTTCAAAA 199
QY 21 AsnAlaAspGlyLysLeuSer-ValLys-PheGlyValLeuPheGlnAspArgCysAla 40
Db 200 AATGCTGATGGAAGTTAAGCCGTGAATTTTGGGTCTCTTCGATGATTAATGTC 259
QY 40 laAsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAla-LysArgArgLysIleVal 59
Db 260 CCAACCTCTTTGAAGCATTTGGTAGGAACCTTTAAAGCTGCAAAACGAAAGGAGATTGTA 319
QY 60 ThrTyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeu 79
Db 320 ACATATCCAGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATTATATACGT 379
QY 80 GlnAsp 81
Db 380 CAAGAT 385

RESULT 3
US-09-252-991A-13298/c
; Sequence 13298, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13298
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13298

Alignment Scores:
Pred. No.: 0.943 Length: 1449
Score: 67.00 Matches: 32
Percent Similarity: 40.00% Conservative: 12
Best Local Similarity: 29.09% Mismatches: 32
Query Match: 16.50% Indels: 34
DB: Gaps: 6

US-09-648-310-2 (1-81) x US-09-252-991A-13298 (1-1449)
QY 3 valGluHisGluValAsnLeuValGluGlu-----IleHis 15
Db 1357 GTTGTACACAGTCCGCGGTACACGCCGGAAGAACGGCTTGGCGCGGAGCCGGCTTCAT 1298
QY 16 ArgLeuGlySerLys-----AsnAlaAspGlyLysLeuSerValLysPheGly 31
Db 1297 CGCGTGGCGCGCGCGCGGTCTCATCAGGAGGCGCGGTCTCGGTCTGCCACAGGT 1238
QY 32 ValLeuPheGlnAspArgCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
Db 1237 GTC-----GACGATCGGCGCGGCGGCGGCGGCTCTCTGTACACTGCCA 1187
QY 52 AlaAlaLys-----ArgArgLysIleValThrTyrAlaGlyGluLeu--- 65
Score: 75
```

Db 1186 GGCTTCGGGTGATCGGCTGCCACCGAACCAGCAGCAGCGAGCGTGGACCGTCGGC 1127
Qy 66 -----LeuLeuGlnGlyValHis----- 71
Db 1126 ACCGCCACCGCGCTTCGCTTCGGCCATCATCGCGGATCGGTCGGCGGGTGTA 1067
Qy 72 AspAspValAspIleValLeuLeuGlnAsp 81
Db 1066 GAGGATGTTGACCTTGCTTGTCGATGAT 1037
RESULT 4
US-09-252-991A-12500
; Sequence 12500, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12500
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12500
Alignment Scores:
Pred. No.: 1.52 Length: 2028
Score: 67.00 Matches: 32
Percent Similarity: 40.00% Conservative: 12
Best Local Similarity: 29.09% Mismatches: 32
Query Match: 16.50% Indels: 34
DB: 4 Gaps: 6
US-09-648-310-2 (1-81) x US-09-252-991A-12500 (1-2028)
Qy 3 ValGluHisGluValAsnLeuValGluGlu-----IleHis 15
Db 655 GTTGTCACCGAGTGGCGGTACACGCCGGAAGACGGCTTGGCGCGAGCGCGCTTCAT 714
Qy 16 ArgLeuGlySerLys-----AsnAlaAspGlyLysLeuSerValLysPheGly 31
Db 715 CGCGTGGCGCGCGCGCGGTTCATCAGCAGCGCGCGGTCTCGGTCTGCCACCGGT 774
Qy 32 ValLeuPheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
Db 775 GTC-----GACGATCGGCGCAGCGCGACTGGCGCGGCTCTCGTAGTACCACTGCCA 825
Qy 52 AlaAlaLys-----ArgArgLysIleValThrTyralaGlyGluLeu--- 65
Db 826 GGCTTCGGGTGATCGGCTGCCACCGAACCAGCAGCAGCGGTGGACCGTCGGC 885
Qy 66 -----LeuLeuGlnGlyValHis----- 71
Db 886 ACCGCCACCGCGCTTCGCTTCGGCCATCATCGCGGATCGGTCGGCGGGTGTA 945
Qy 72 AspAspValAspIleValLeuLeuGlnAsp 81
Db 946 GAGGATGTTGACCTTGCTTGTCGATGAT 975
RESULT 5
US-09-252-991A-12977/c
; Sequence 12977, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12977
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12977
Alignment Scores:
Pred. No.: 1.53 Length: 2040
Score: 67.00 Matches: 32
Percent Similarity: 40.00% Conservative: 12
Best Local Similarity: 29.09% Mismatches: 32
Query Match: 16.50% Indels: 34
DB: 4 Gaps: 6
US-09-648-310-2 (1-81) x US-09-252-991A-12977 (1-2040)
Qy 3 ValGluHisGluValAsnLeuValGluGlu-----IleHis 15
Db 1437 GTTGTCACCGAGTGGCGGTACACGCCGGAAGACGGCTTGGCGCGAGCGCGCTTCAT 1378
Qy 16 ArgLeuGlySerLys-----AsnAlaAspGlyLysLeuSerValLysPheGly 31
Db 1377 CGCGTGGCGCGCGCGCGGTTCATCAGCAGCGCGCGGTCTCGGTCTGCCACCGGT 1318
Qy 32 ValLeuPheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
Db 1317 GTC-----GACGATCGGCGCAGCGCGACTGGCGCGGCTCTCGTAGTACCACTGCCA 1267
Qy 52 AlaAlaLys-----ArgArgLysIleValThrTyralaGlyGluLeu--- 65
Db 1266 GGCTTCGGGTGATCGGCTGCCACCGAACCAGCAGCAGCGGTGGACCGTCGGC 1207
Qy 66 -----LeuLeuGlnGlyValHis----- 71
Db 1206 ACCGCCACCGCGCTTCGCTTCGGCCATCATCGCGGATCGGTCGGCGGGTGTA 1147
Qy 72 AspAspValAspIleValLeuLeuGlnAsp 81
Db 1146 GAGGATGTTGACCTTGCTTGTCGATGAT 1117
RESULT 6
US-09-252-991A-12137
; Sequence 12137, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12137
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12137
Alignment Scores:
Pred. No.: 0.178 Length: 393

Score: 66.50 Matches: 23
Percent Similarity: 43.21% Conservative: 12
Best Local Similarity: 28.40% Mismatches: 35
Query Match: 16.38% Indels: 11
DB: 4 Gaps: 3

US-09-648-310-2 (1-81) x US-09-252-991A-12137 (1-393)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerIys 20
DB 136 ATGAAGGACACACAGCACTCAACCCATCCGATCTGTGAGCGGCTG-----AAA 189
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
DB 190 CGCGCGGATGTCATCTTCGGCACGCTCATAGGATGATCGAAAGTGGCGAATCCTGTCTC 249
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
DB 250 GACATCGCCGCGACGCTCCGCGGTGGAAGCGG-----GTGACG 291
QY 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspValLeuLeuGln 80
DB 292 GCCGAAAGCGGCTCTG-----ATCCAGCACACATCGACCATTCCTGCGCCAT 342
QY 81 Asp 81
DB 343 GAC 345

RESULT 7

US-09-313-294A-4253/c
; Sequence 4253, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1993-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4253
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348078H1
; LOCATION: 14, 266, 310, 315, 317, 410, 414
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4253

Alignment Scores:
Pred. No.: 0.337 Length: 421
Score: 65.00 Matches: 24
Percent Similarity: 46.88% Conservative: 6
Best Local Similarity: 37.50% Mismatches: 24
Query Match: 16.01% Indels: 10
DB: 4 Gaps: 3

US-09-648-310-2 (1-81) x US-09-313-294A-4253 (1-421)

QY 2 AsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeu----- 17
DB 219 ATCTTGACGACCGCGGCTCTCTGTAGATGAACCCGAGATGCGCTTGACGCGC 160
QY 18 ---GlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAsp 36
DB 159 CCTTCTTCGCCAACTCGGATCGCGGCTGTGTGATGCCCTGTGATGTTGTACACGAC 100
QY 37 AspArgCysAlaAsnLeuPheGluAlaLeuValGlyThr-----LeuLysAlaAla 53

DB 99 TTGCGGTGGCT-----TGCAGCGCCCTTGCCAGACCTTCCCGCCCTTCCCGCGGCC 46
QY 54 LysArgArgLys 57
DB 45 AGACATCGCGCA 34

RESULT 8

US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc.feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g

```

; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature

```

```

; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664854)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1
; US-09-648-310-2 (1-81) x US-08-916-421B-1 (1-1664976)
Alignment Scores:
Pred. No.: 4.22e+04
Score: 65.00
Percent Similarity: 49.25%
Best Local Similarity: 26.87%
Query Match: 16.01%
DB: 4
Length: 1664976
Matches: 18
Conservative: 15
Mismatches: 20
Indels: 14
Gaps: 3
Qy 3 ValGluHisGluValAsn-----LeuLeuValGluGluLeuHisArgLeuGlySer 19
Db 720607 ATTGAGCATAGGTTAGAGATGCGCTTTTGTGTCAGAAATGCTAATGCCGTGGT--- 720551
Qy 20 LysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCys 39
Db 720550 -----AGAAATGCTTATTGCTGATGATGATGATGCTTAGAAGATGATGATGC 720497
Qy 40 AlaAsnLeu-----PheGluAlaLeuValGlyThrLeuLys 51
Db 720496 ATAAAGATAGGTAATCAATCCATGGAGTATATAAAGAACTTAATCAATGAACCTTAA 720437
Qy 52 AlaAlaLysArgGlyLysIle 58
Db 720436 AGTGTTAACTAAAAAATTA 720416
RESULT 9
US-09-328-352-1774
; Sequence 1774, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

```

;; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: GTC99-03PA

;; CURRENT APPLICATION NUMBER: US/09/328,352

;; CURRENT FILING DATE: 1999-06-04

;; NUMBER OF SEQ ID NOS: 8252

;; SEQ ID NO 1774

;; LENGTH: 2133

;; TYPE: DNA

;; ORGANISM: Acinetobacter baumannii

US-09-328-352-1774

Alignment Scores:

Pred. No.: 4.85 Length: 2133
Score: 64.00 Matches: 21
Percent Similarity: 53.03% Conservative: 14
Best Local Similarity: 31.82% Mismatches: 23
Query Match: 15.76% Indels: 8
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-328-352-1774 (1-2133)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20

DB 1396 ATGGTGGTACCGCGTGAACACAACTGGTGCCTTATGTCAT---TTAGGAACGGGT 1452

QY 21 Asn-----AlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAsp--- 36

DB 1453 AACTACCATGCTATGATGCTGCGATTTATCTACTGATTACGGCCTAATGACCACCGATAAA 1512

QY 37 AspArgCysAlaAsn-----LeuPheGluAlaLeuValGlyThrLeuLysAlaAla 53

DB 1513 GACTGTGTGAAGACGTACACCGTATTTTCCAGAGCTCACGGGTATGGGTAAATGGCA 1572

QY 54 LysArgArgLysIleVal 59

DB 1573 AAACGTAAAAAGTTACTC 1590

RESULT 10

US-09-252-991A-8104/c

;; Sequence 8104, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; PRIOR FILING DATE: 1999-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 8104

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8104

Alignment Scores:

Pred. No.: 2.37 Length: 1134
Score: 63.50 Matches: 26
Percent Similarity: 41.03% Conservative: 6
Best Local Similarity: 33.33% Mismatches: 21
Query Match: 15.64% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8104 (1-1134)

QY 14 IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33

DB 775 GTTCATCGC-----CAGCGCGATGGGAACCTGCCGCGAGTCCTCGCGTAGAC 728

QY 34 PheGlnAspArgCysAlaAsnLeuPheGluAlaLeu----- 46

DB 727 GCGGATGATCGACAGGGTCCGCGCTTGGCCAGGCGCTCCACGCCACTCCAGGCGCTG 668

QY 47 -----ValGlyThrLeuLysAlaAlaLysArgArgLysIle 58

DB 667 TCGCGGGCGGCTTCCCGGACTCCAGCTGCTGCTCTCTGCGCGCGCGCGGT----- 614

QY 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValasp 75

DB 613 -----GCGGTGCCATGCTGTCTCGCGCTCCACGCCAGCGCGTCGAT 569

RESULT 11

US-09-252-991A-8001/c

;; Sequence 8001, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; PRIOR FILING DATE: 1999-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 8001

;; LENGTH: 1314

;; TYPE: DNA

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-8001

Alignment Scores:

Pred. No.: 2.92 Length: 1314
Score: 63.50 Matches: 26
Percent Similarity: 41.03% Conservative: 6
Best Local Similarity: 33.33% Mismatches: 21
Query Match: 15.64% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8001 (1-1314)

QY 14 IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33

DB 1023 GTTCATCGC-----CAGCGCGATGGGAACCTGCCGCGAGTCCTTCGCGTAGAC 976

QY 34 PheGlnAspArgCysAlaAsnLeuPheGluAlaLeu----- 46

DB 975 GCGGATGATCGACAGGGTCCGCGCTTGGCCAGGCGCTCCACGCCACTCCAGGCGCTG 916

QY 47 -----ValGlyThrLeuLysAlaAlaLysArgArgLysIle 58

DB 915 TCGCGGGCGGCTTCCCGGACTCCAGCTGCTGCTCTCTGCGCGCGCGCGGT----- 862

QY 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValasp 75

DB 861 -----GCGGTGCCATGCTGTCTCGCGCTCCACGCCAGCGCGTCGAT 817

RESULT 12

US-09-252-991A-8133

;; Sequence 8133, Application US/09252991A

;; Patent No. 6551795

;; GENERAL INFORMATION:

;; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; PRIOR FILING DATE: 1999-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR FILING DATE: 1998-02-18

```

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8133
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8133

Alignment Scores:
Pred. No.: 4,4 Length: 1755
Score: 63,50 Matches: 26
Percent Similarity: 41,03% Conservative: 6
Best Local Similarity: 33,33% Mismatches: 21
Query Match: 15,64% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8133 (1-1755)
Qy 14 IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33
Db 1279 GTTCATCGC-----CAGGCCGATGGGAAACTGCCCGAGTCTTCGGCGTAGAC 1326
Qy 34 PheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeu----- 46
Db 1327 GCGGATGATCGACAGGCTCCGGCTTGCCAGGCCCTGCACGCCCACTCCAGGCGCTG 1386
Qy 47 -----ValGlyThrLeuLysAlaAlaLysArgGlyIle 58
Db 1387 TGGCGGGGGGTTGCCGGGACTCCAGCTGTGTCCTCTCGCGCGCGCGCGGT----- 1440
Qy 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp 75
Db 1441 -----GGCGTGCCATGCTGTGCTCGCGGTCCAGCGCGCGGTGCAT 1485

RESULT 13
US-09-252-991A-13643/c
; Sequence 13643, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13643
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13643

Alignment Scores:
Pred. No.: 2,51 Length: 1038
Score: 63,00 Matches: 18
Percent Similarity: 64,10% Conservative: 7
Best Local Similarity: 46,15% Mismatches: 8
Query Match: 15,52% Indels: 6
DB: 4 Gaps: 2

US-09-648-310-2 (1-81) x US-09-252-991A-13643 (1-1038)
Qy 42 LeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyr 61
Db 720 CTTTCCGGGCGCTTCTCGGTGTTCTC---GCCGAATACCGTCAGCGTACGTTGTTATTC 664
Qy 62 AlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8133
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8133

Alignment Scores:
Pred. No.: 4,4 Length: 1755
Score: 63,50 Matches: 26
Percent Similarity: 41,03% Conservative: 6
Best Local Similarity: 33,33% Mismatches: 21
Query Match: 15,64% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8133 (1-1755)
Qy 14 IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33
Db 1279 GTTCATCGC-----CAGGCCGATGGGAAACTGCCCGAGTCTTCGGCGTAGAC 1326
Qy 34 PheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeu----- 46
Db 1327 GCGGATGATCGACAGGCTCCGGCTTGCCAGGCCCTGCACGCCCACTCCAGGCGCTG 1386
Qy 47 -----ValGlyThrLeuLysAlaAlaLysArgGlyIle 58
Db 1387 TGGCGGGGGGTTGCCGGGACTCCAGCTGTGTCCTCTCGCGCGCGCGCGGT----- 1440
Qy 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp 75
Db 1441 -----GGCGTGCCATGCTGTGCTCGCGGTCCAGCGCGCGGTGCAT 1485

RESULT 13
US-09-252-991A-13643/c
; Sequence 13643, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13643
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13643

Alignment Scores:
Pred. No.: 2,51 Length: 1038
Score: 63,00 Matches: 18
Percent Similarity: 64,10% Conservative: 7
Best Local Similarity: 46,15% Mismatches: 8
Query Match: 15,52% Indels: 6
DB: 4 Gaps: 2

US-09-648-310-2 (1-81) x US-09-252-991A-13643 (1-1038)
Qy 42 LeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyr 61
Db 720 CTTTCCGGGCGCTTCTCGGTGTTCTC---GCCGAATACCGTCAGCGTACGTTGTTATTC 664
Qy 62 AlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80

```

```

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8133
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8133

Alignment Scores:
Pred. No.: 4,4 Length: 1755
Score: 63.50 Matches: 26
Percent Similarity: 41.0% Conservative: 6
Best Local Similarity: 33.3% Mismatches: 21
Query Match: 15.6% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8133 (1-1755)
Qy 14 IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33
Db 1279 GTTATCGC-----CAGCCGATGGAACATGCCCGAGTCTTCGGCGTAGAC 1326
Qy 34 PheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeu----- 46
Db 1327 GCGATGATCGACAGGTCGCGCTTGCCAGGCCCTGCACGCCCACTCCAGGCGCTG 1386
Qy 47 -----ValGlyThrLeuLysAlaAlaLysArgGlyIle 58
Db 1387 TGGCGGGGGGTTGCCGGGACTCCAGCTGTGTGCCCTCTGGCGCGCGCGGGT----- 1440
Qy 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp 75
Db 1441 -----GGCGTGCCATGCTGTGTGCTGCGCGTCCAGCGCGGCTGCAT 1495

RESULT 13
US-09-252-991A-13643/c
; Sequence 13643, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13643
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13643

Alignment Scores:
Pred. No.: 2,51 Length: 1038
Score: 63.00 Matches: 18
Percent Similarity: 64.10% Conservative: 7
Best Local Similarity: 46.15% Mismatches: 8
Query Match: 15.52% Indels: 6
DB: 4 Gaps: 2

US-09-648-310-2 (1-81) x US-09-252-991A-13643 (1-1038)
Qy 42 LeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyr 61
Db 720 CTTTCCGGGCGCTTCTCGGTGTTCTC---GCCGAATACCGTCAGCGTACGTTGTTATTC 664
Qy 62 AlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8133
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-8133

Alignment Scores:
Pred. No.: 4,4 Length: 1755
Score: 63.50 Matches: 26
Percent Similarity: 41.0% Conservative: 6
Best Local Similarity: 33.3% Mismatches: 21
Query Match: 15.6% Indels: 25
DB: 4 Gaps: 4

US-09-648-310-2 (1-81) x US-09-252-991A-8133 (1-1755)
Qy 14 IleHisArgLeuGlySerLysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeu 33
Db 1279 GTTATCGC-----CAGCCGATGGAACATGCCCGAGTCTTCGGCGTAGAC 1326
Qy 34 PheGlnAspAspArgCysAlaAsnLeuPheGluAlaLeu----- 46
Db 1327 GCGATGATCGACAGGTCGCGCTTGCCAGGCCCTGCACGCCCACTCCAGGCGCTG 1386
Qy 47 -----ValGlyThrLeuLysAlaAlaLysArgGlyIle 58
Db 1387 TGGCGGGGGGTTGCCGGGACTCCAGCTGTGTGCCCTCTGGCGCGCGCGGGT----- 1440
Qy 59 ValThrTyrAlaGlyGluLeuLeuGlnGlyValHis---AspAspValAsp 75
Db 1441 -----GGCGTGCCATGCTGTGTGCTGCGCGTCCAGCGCGGCTGCAT 1495

RESULT 13
US-09-252-991A-13643/c
; Sequence 13643, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13643
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13643

Alignment Scores:
Pred. No.: 2,51 Length: 1038
Score: 63.00 Matches: 18
Percent Similarity: 64.10% Conservative: 7
Best Local Similarity: 46.15% Mismatches: 8
Query Match: 15.52% Indels: 6
DB: 4 Gaps: 2

US-09-648-310-2 (1-81) x US-09-252-991A-13643 (1-1038)
Qy 42 LeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyr 61
Db 720 CTTTCCGGGCGCTTCTCGGTGTTCTC---GCCGAATACCGTCAGCGTACGTTGTTATTC 664
Qy 62 AlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80

```

```
; * PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/593,691
; FILING DATE: 26-MAR-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12176-5-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 361..2043
; US-08-358-901-1

Alignment Scores:
Pred. No.: 9.42 Length: 2323
Score: 62.50 Matches: 19
Percent Similarity: 52.94% Conservative: 17
Best Local Similarity: 27.94% Mismatches: 31
Query Match: 15.39% Indels: 1
DB: 1 Gaps: 1

US-09-648-310-2 (1-81) x US-08-358-901-1 (1-2323)
QY 5 HisGluValAsnLeuValGluGluIleHisArgLeuGlySerLysAsnAlaAspGly 24
Db 1086 CACGCCCTTCTCGGCTTTTGACGCGCGACGATCGTGGATCGAGATTGAA--- 1030
QY 25 LysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAlaAsnLeuPheGlu 44
Db 1029 GTCTCGCGGCTTGGCAGGAGCGCTGCAAGCCTGGAAGCTGCTTCAATCTCTTCAG 970
QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThrTyrAlaGlyGlu 64
Db 969 GCTGCTGTGATGCGCATTTGCCCGCCAGATCGGATAAAGCCGTACAGCGTGGTCAG 910
QY 65 LeuLeuLeuGlnGlyValHisAsp 72
Db 909 GTTTGCGCGGGATCTTGTGAC 886
```

Search completed: September 1, 2004, 22:11:22
Job time : 233 secs


```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: September 1, 2004, 21:55:40 ; Search time 263.5 Seconds
        (without alignments)
        1512.848 Million cell updates/sec

Title: US-09-648-310-2
Perfect score: 406
Sequence: 1 MNVEHEVNVLLVEIHRIGSK.....AGELLQGVHDDVIDVLLQD 81

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09648310/runat_27082004_154408_27994/app_query.fasta_1.526
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HPASITZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09648310@cgn1_1_953@runat_27082004_154408_27994
-NCPU=6 -ICPU=3 -NO_XMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

```

SUMMARIES
Result      %
No.  Score Match Length DB ID Description

```

```

1 406 100.0 780 13 US-10-373-556-1 Sequence 1, Appli
2 406 100.0 780 13 US-10-373-556-5 Sequence 5, Appli
3 390 96.1 400 13 US-10-085-783A-21733 Sequence 21733, A
4 390 96.1 400 13 US-10-085-783A-21733 Sequence 21733, A
5 390 96.1 400 16 US-10-242-535A-21733 Sequence 56189, A
6 390 96.1 483 13 US-10-085-783A-56189 Sequence 56189, A
7 390 96.1 483 16 US-10-242-535A-56189 Sequence 56189, A
8 390 96.1 527 12 US-09-969-034-557 Sequence 557, App
9 390 96.1 778 9 US-09-925-300-557 Sequence 545, App
10 390 96.1 835 13 US-10-373-556-3 Sequence 3, Appli
11 390 96.1 835 13 US-10-373-556-6 Sequence 6, Appli
12 390 96.1 876 13 US-10-342-887-156 Sequence 156, App
13 390 96.1 876 13 US-10-172-118-156 Sequence 156, App
14 384 94.6 717 12 US-09-969-034-750 Sequence 750, App
15 386 95.1 594 12 US-09-969-034-748 Sequence 748, App
16 368 90.6 458 10 US-09-918-995-36075 Sequence 26075, A
17 351 86.5 800 17 US-10-725-969A-26 Sequence 26, Appl
18 302 74.4 533 13 US-10-641-643-79 Sequence 79, Appl
19 286 70.4 486 9 US-09-938-842A-355 Sequence 19867, A
20 286 70.4 486 11 US-09-938-842A-355 Sequence 355, App
21 286 70.4 492 10 US-09-770-961-618 Sequence 618, App
22 282 69.5 818 17 US-10-437-963-43648 Sequence 43648, A
23 272 67.0 716 13 US-10-424-599-94878 Sequence 94878, A
24 237 58.4 268 9 US-09-924-093B-2020 Sequence 2020, Ap
25 236 58.1 552 9 US-09-920-300A-939 Sequence 939, App
26 236 58.1 552 14 US-10-033-528-939 Sequence 939, App
27 236 58.1 552 15 US-10-093-926-939 Sequence 939, App
28 208 51.2 388 9 US-09-925-293-318 Sequence 318, App
29 208 51.2 388 10 US-09-925-299-318 Sequence 318, App
30 153 38.9 289 9 US-09-294-093B-4150 Sequence 4150, Ap
31 113 27.8 388 16 US-10-191-803-820 Sequence 820, App
32 109 26.1 1128 17 US-10-644-659A-3 Sequence 3, Appli
33 106 26.1 1146 17 US-10-644-659A-1 Sequence 1, Appli
34 106 26.1 1322 16 US-10-104-047-1199 Sequence 1199, Ap
35 98 24.1 60 10 US-09-908-975-22102 Sequence 22102, A
36 96.5 23.8 489 17 US-10-644-659A-7 Sequence 7, Appli
37 89 21.9 175 9 US-09-294-093B-5438 Sequence 5438, Ap
38 72.5 17.9 2960 17 US-10-437-963-34365 Sequence 34365, A
39 71 17.5 1728 13 US-10-282-132A-16022 Sequence 16022, A
40 69.5 17.1 1284 13 US-10-282-132A-39648 Sequence 39648, A
41 69.5 17.1 3806 13 US-09-854-867-62 Sequence 62, Appl
42 68.5 16.9 1107 13 US-10-425-114-33343 Sequence 3343, A
43 68.5 16.9 1257 13 US-10-282-122A-14898 Sequence 14898, A
44 68.5 16.9 2163 13 US-10-425-114-30828 Sequence 30828, A
45 66 16.3 321491 13 US-10-087-192-532 Sequence 532, App

```

ALIGNMENTS

```

RESULT 1
US-10-373-556-1
; Sequence 1, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 780
; TYPE: DNA
; ORGANISM: rattus norvegicus

```

US-10-373-556-1

Alignment Scores:

Alignment Scores:		
Pred. No.:	3.9e-56	Length: 780
Score:	406.00	Matches: 81
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	13	Gaps: 0

US-09-648-310-2 (1-81) X US-10-373-556-1 (1-780)

Qy		1	MetAsnValGluHisGluValAsnLeuLeuValGluGluLeHisArgIeuGlySerIys	20
Db		170	ATGAACCGTGGAGCATGAGGTAACTCTGCTGGAGGAAAATTCATCGTCTGGGTTCCAA	229
Qy		21	AsnAlaAspGlyLyLeuSerValIyPheGlyValLeuPheGlnAspAspArgCySAla	40
Db		230	AATGCCGATGGAAACTGAGTGTAAGTTTGGGGTCTCTTCCAAGCAGCAGATGTGCC	289
Qy		41	AsnLeuPheGluAlaLeuValGIYThrieuLySaLaAlalySargIySleValThr	60
Db		290	AATCTCTTTGAAGCGTTGGTGGGAACCTCGAAGCCGCAAAACGAAGGAAGATTGTTACG	349
Qy		61	TyrAlaGlyGluLeuLeuGlnClvVaiHiSaSpValAspIleValLeuLeuGln	80
Db		350	TACGCAGGAGAGCTCTTTTCAAAGGTGTCATGATGATTTGACATTTGTATTGCTGC	409
Qy		81	Asp	81
Db		410	GAT	412

RESULT 2

```

US-10-373-556-5
; Sequence 5, Application US/10373556
; Publication No. US2003024402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 780
; TYPE: DNA
; ORGANISM: rattus norvegicus
US-10-373-556-5

```

Alignment Scores:

Alignment Scores:		
Pred. No.:	3.9e-56	Length: 780
Score:	406.0%	Matches: 81
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	13	Gaps: 0

US-09-648-310-2 (1-81) x US-10-373-556-5 (1-780)

QY	1	Met	Asn	Val	Glu	His	Glu	Val	Asn	Leu	Val	Glu	Leu	His	Arg	Leu	Gly	Ser	Leu	20
Db	170	AT	GA	CT	GG	AG	CA	TAG	GT	TAA	CT	CT	GG	TGG	AG	GA	TTC	AT	CT	CT
QY	21	Asn	Ala	Asp	Gly	Leu	Ser	Val	Lys	Phe	Gly	Val	Leu	Phe	Gln	Asp	Arg	Cys	Ala	40

Db	230	AATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCTCTTCCAAAGACGACAGATCTGCC	288
Qy	41	AsnLeuPheGluAlaLeuValGlyThrLeuValaalaalalysargarglystlleValThr	60
Db	290	AATCTCTTTGAAGCGTTGGTGGGAACCTGAAGCCGCAAAACGAAGGAAGATTGTACG	349
Qy	61	TyrAlaGlyGluLeuLeuLeuGlnGlyValHisAspValAspileValLeuLeuGln	80
Db	350	TACGCAGCAGAGCTGCTTTTCGAAGGTGTTCAATGATGATGTTGATTGCTGCAA	409
Qy	81	Asp	81
Db	410	GAT	412
RESULT 3			
US-10-085-783A-21733			
; Sequence 21733, Application US/10085783A			
; Publication No. US20040037841A1			

RESULT 3

```

US-10-085-783A-21733
; Sequence 21733, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 21733
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (48)..(48)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (328)..(328)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-21733

```

Alignment Scores:

Alignment Scores:			
Pred. No.:	6.04e-54	Length:	400
Score:	390.00	Matches:	76
Percent Similarity:	98.77%	Conservative:	4
Best Local Similarity:	93.83%	Mismatches:	1
Query Match:	96.0%	Indels:	0
DB:	13	Gaps:	0

US-09-648-310-2 (1-81) x US-10-085-783A-21733 (1-400)

1	Met	Asn	Val	Glu	Hu	I	S	G	U	Val	Asn	Leu	Val	G	U	L	I	L	E	H	S	A	R	G	L	E	U	G	I	S	Y	20
...		
77	AT	GA	TG	TG	AT	C	A	C	G	A	G	T	T	A	C	C	T	T	A	G	T	G	A	G	A	A	T	T	C	A	A	136
21	Asn	Ala	Asp	G	L	Y	S	Leu	Ser	Val	L	Y	S	P	H	e	C	L	Y	Val	Leu	P	h	e	C	L	N	A	S	P	A	40
...		
137	AAT	GT	GAT	G	A	A	AGT	T	A	AG	CGT	C	A	A	T	T	T	G	G	G	T	C	T	C	T	C	G	T	G	A	T	196
41	Asn	Leu	P	h	e	G	L	U	A	L	Leu	V	a	L	G	I	Y	T	h	r	Leu	L	Y	S	A	L	A	L	Y	S	A	60
197	AAC	CT	T	T	T	GA	CA	T	T	G	T	AG	AA	CT	T	T	T	AA	AG	CT	T	T	AA	AG	CT	T	T	AA	AG	AA	256	

Qy	81	Asp	81
Db	317	GAT	319

RESULT 5
US-10-085-783A-56189
; Sequence 56189, App

```

; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods

```

```

; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340

```

; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12

; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994

```

; SEQ ID NO 56189
; LENGTH: 483

```

ORGANISM: Human
US-10-085-783A-56189

Alignment Scores:
Pred. No.: 7.97e-54
Matches: 390 00
Length

Percent Similarity:
Best Local Similarity
Query Match.

DB:
US-09-648-310-2 (1-81

Qy 1 MetAsnV

81 ATGAATC
21 AsnAlaA

Db 141 AATGCTC

Qy	41	AsnLeuPheGluAlaLeuValGlyThrLeuIysAlaAlaIysAsGArgLysIleValaThr	60
Db	201	AACTCTTTGACGATTTGGTAGGAACCTCTTAAAGCTGCAAAACGAAGGAATTTGAACA	260
Qy	61	TyrAlaGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleValLeuLeuGln	80
Db	261	TATCCAGGAGAGCTGCTCTTCGACAGGTGTTCAATGATGTTTGACATTTATTACTGCA	320

Qy 81 Asp 81

Db 321 GAT 323
 RESULT 6

US-10-242-333A-36189
; Sequence 56189, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:

; APPLICANT: CINCORP INC.
 ; APPLICANT: LIEW, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005

; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ;

; PRIOR APPLICATION NUMBER: US 60/303,340

```
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 56189
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-56189

Alignment Scores:
Pred. No.: 7,97e-54 Length: 483
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 16 Gaps: 0

US-09-648-310-2 (1-81) x US-10-242-535A-56189 (1-483)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 81 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGGAAATTCATCGTTGGTTCAAAA 140
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
Db 141 AATGCTGATGGAAGTTAAGCTGAAATTTGGGTCCTCTCCGTGATGATAATGTGCC 200
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLeuValThr 60
Db 201 AACCTCTTTGAAGCATTTGTAGGAATCTTTAAAGCTGCAAAACGAAGGATTGTACA 260
QY 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspValLeuLeuGln 80
Db 261 TATCCAGGAGAGCTGCTTCGCAAGGTTCATGATGATGATGATGATGATGATGATGCA 320

QY 81 Asp 81
Db 321 GAT 323

RESULT 7
US-09-969-034-557/c
; Sequence 557, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 557
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 503-512, 539, 596, 620
; OTHER INFORMATION: n = A,T,C or G

US-09-969-034-557
Alignment Scores:
Pred. No.: 1.17e-53 Length: 627
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 12 Gaps: 0

US-09-648-310-2 (1-81) x US-09-969-034-557 (1-627)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 271 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGGAAATTCATCGTTGGTTCAAAA 212
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspArgCysAla 40
Db 211 AATGCTGATGGAAGTTAAGCTGAAATTTGGGTCCTCTCCGTGATGATAATGTGCC 152
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLeuValThr 60
Db 151 AACCTCTTTGAAGCATTTGTAGGAATCTTTAAAGCTGCAAAACGAAGGATTGTACA 92
QY 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspValLeuLeuGln 80
Db 91 TATCCAGGAGAGCTGCTTCGCAAGGTTCATGATGATGATGATGATGATGATGCA 32

QY 81 Asp 81
Db 31 GAT 29

RESULT 8
US-09-925-300-545
; Sequence 545, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 545
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (641)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (652)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-545

Alignment Scores:
Pred. No.: 1.61e-53 Length: 778
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 9 Gaps: 0

US-09-648-310-2 (1-81) x US-09-925-300-545 (1-778)

QY 1 MetAsnValGluHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
```

```

186 ATGAATGGATCAGGATTAACTCTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 245
21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
246 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGATGATGATAATGTGCC 305
41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
306 AACCTCTTTGAAGCATTTGGTAGGAACCTTTAAAGCTGCAAAACGAAAGAGATTGTAA 365
61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
366 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGATGATGATGATGATGATG 425
81 Asp 81
426 GAT 428

RESULT 9
US-10-373-556-3
; Sequence 3, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 835
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-373-556-3

Alignment Scores:
Pred. No.: 1.78e-53 Length: 835
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 13 Gaps: 0

US-09-648-310-2 (1-81) x US-10-373-556-3 (1-835)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 197 ATGAATGGATCAGGATTAACTCTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 256
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGATGATGATAATGTGCC 316
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 317 AACCTCTTTGAAGCATTTGGTAGGAACCTTTAAAGCTGCAAAACGAAAGAGATTGTAA 376
Qy 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
Db 377 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGATGATGATGATGATG 436
81 Asp 81
437 GAT 439

RESULT 11
US-10-342-887-156
; Sequence 156, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
```

```

186 ATGAATGGATCAGGATTAACTCTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 245
21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
246 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGATGATGATAATGTGCC 305
41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
306 AACCTCTTTGAAGCATTTGGTAGGAACCTTTAAAGCTGCAAAACGAAAGAGATTGTAA 365
61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
366 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGATGATGATGATGATGATG 425
81 Asp 81
426 GAT 428

RESULT 9
US-10-373-556-6
; Sequence 6, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 835
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-373-556-6

Alignment Scores:
Pred. No.: 1.78e-53 Length: 835
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 96.06% Indels: 0
DB: 13 Gaps: 0

US-09-648-310-2 (1-81) x US-10-373-556-6 (1-835)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys 20
Db 197 ATGAATGGATCAGGATTAACTCTTAGTGAGGAAATTCATCGTTTGGGTTCAAAA 256
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGTCCTCTTCGATGATGATAATGTGCC 316
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 317 AACCTCTTTGAAGCATTTGGTAGGAACCTTTAAAGCTGCAAAACGAAAGAGATTGTAA 376
Qy 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuGln 80
Db 377 TATCCAGGAGAGCTGCTTCTGCAAGGTTCATGATGATGATGATGATGATGATG 436
81 Asp 81
437 GAT 439

RESULT 11
US-10-342-887-156
; Sequence 156, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
```



```
Db 199 ATGAATGTGGATCAGCAGGTTAACTCTTAGTGGAGAAATTCATCGTTGGTTCAAAA 258
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 259 AATGCTGATGGAAGTTACCGTGAATTTGGGGTCTCTTCGATGATATAAATGTGCC 318
Qy 41 AsnLeuPheGlnAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 319 AACCTCTTTGAAGCAATTTGGTAGGAATCTTTAAAGCTGCAAAACGAAGAGATTGTAACA 378
Qy 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeuGln 80
Db 379 TATCCAGAGAGTGTCTTACAGGNGTTCATGATGATGTGACATATATATTACTGCAA 438
Qy 81 Asp 81
Db 439 GAA 441

RESULT 14
US-09-969-034-748
; Sequence 748, Application US/09969034
; Publication No. US2004011068A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Carino, Theodore J.
; APPLICANT: Deivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 452, 481, 482, 505, 521, 536, 540, 594, 599, 607, 635, 641,
; LOCATION: 643, 657, 664, 673, 691, 695, 700
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-748

Alignment Scores:
Pred. No.: 1.37e-52 Length: 717
Score: 384.00 Matches: 75
Percent Similarity: 98.75% Conservative: 4
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 94.58% Indels: 0
DB: 12 Gaps: 0

US-09-648-310-2 (1-81) x US-09-969-034-748 (1-717)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20
Db 202 ATGAATGTGGATCAGCAGGTTAACTCTTAGTGGAGAAATTCATCGTTGGTTCAAAA 261
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 262 AATGCTGATGGAAGTTACCGTGAATTTGGGGTCTCTTCGATGATATAAATGTGCC 321
Qy 41 AsnLeuPheGlnAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 322 AACCTCTTTGAAGCAATTTGGTAGGAATCTTTAAAGCTGCAAAACGAAGAGATTGTAACA 381
```

```
Qy 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeuGln 80
Db 382 TATCCAGAGAGTGTCTTACAGGNGTTCATGATGATGTGACATATATATTACTGCAA 441

RESULT 15
US-09-918-995-26075
; Sequence 26075, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26075
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(458)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26075

Alignment Scores:
Pred. No.: 2.92e-50 Length: 458
Score: 368.00 Matches: 72
Percent Similarity: 98.68% Conservative: 3
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 90.64% Indels: 0
DB: 10 Gaps: 0

US-09-648-310-2 (1-81) x US-09-918-995-26075 (1-458)
Qy 1 MetAsnValGluHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20
Db 231 ATGAATGTGGATCAGCAGGTTAACTCTTAGTGGAGAAATTCATCGTTGGTTCAAAA 290
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheGlnAspAspArgCysAla 40
Db 291 AATGCTGATGGAAGTTAAAGCGTGAATTTGGGGTCTCTTCGATGATATAAATGTGCC 350
Qy 41 AsnLeuPheGlnAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 351 AACCTCTTTGAAGCAATTTGGTAGGAATCTTTAAAGCTGCAAAACGAAGAGATTGTAACA 410
Qy 61 TyrAlaGlyGluLeuLeuGlnGlyValHisAspValAspIleValLeuLeuGln 76
Db 411 TATCCAGAGAGTGTCTTTCGAAGGTTTCATGATGATGTGACATT 458

Search completed: September 2, 2004, 00:01:59
Job time : 265.5 secs
```

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 1, 2004, 20:15:24 ; Search time 61 Seconds
(without alignments)
736.902 Million cell updates/sec

Title: US-09-648-310-4
Perfect score: 410
Sequence: 1 MNVDHEVNLVEEHRIGSK.....PGELLOGVHDVDDIILLQD 81

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlpl
-O=/cgn2_1/USPTO spool_p/US09648310/runat_27082004_154406_27960/app_query.fasta_1.526
-DB=Issued Patents NA -OPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LCOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09648310@cgn2_1_141_@runat_27082004_154406_27960 -NCPU=6 -ICPU=3
-NO MNAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	371	90.5	786	4	US-09-023-655-79 Sequence 79, Appl
2	352	85.9	800	4	US-09-644-460-26 Sequence 26, Appl
3	66	16.1	2133	4	US-09-328-352-1774 Sequence 1774, Ap
4	64.5	15.7	393	4	US-09-252-991A-12137 Sequence 12137, A
5	64.5	15.7	2323	1	US-08-358-901-1 Sequence 1, Appli
6	64.5	15.7	2323	1	US-08-566-347-1 Sequence 1, Appli
7	64.5	15.7	2323	1	US-08-693-835-1 Sequence 1, Appli
8	64	15.6	2329	1	US-08-457-797A-8 Sequence 8, Appli
9	64	15.6	2329	1	US-08-812-025-8 Sequence 8, Appli
10	64	15.6	2329	3	US-09-138-873A-8 Sequence 8, Appli
11	63	15.4	1278	4	US-09-134-000C-2571 Sequence 2571, Ap
12	63	15.4	14770	4	US-09-220-132-30 Sequence 30, Appli

62.5	15.2	675	4	US-09-252-991A-5194	Sequence 5194, Ap
62.5	15.2	954	4	US-09-252-991A-5307	Sequence 5307, Ap
62	15.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
61	14.9	885	4	US-09-328-352-1423	Sequence 1423, Ap
61	14.9	1074	1	US-08-008-216-3	Sequence 3, Appli
61	14.9	1074	1	US-08-459-569-3	Sequence 3, Appli
61	14.9	1074	1	US-08-458-831-3	Sequence 3, Appli
61	14.9	1074	1	US-08-458-831-3	Sequence 1659, Ap
61	14.9	1385	4	US-09-107-532A-1659	Sequence 192, App
61	14.9	6563	4	US-09-453-702B-192	Sequence 19, Appl
61	14.9	21126	1	US-08-008-216-19	Sequence 19, Appl
61	14.9	21126	1	US-08-459-569-19	Sequence 19, Appl
61	14.9	21126	1	US-08-458-831-19	Sequence 12508, A
60.5	14.8	2082	4	US-09-107-532A-2158	Sequence 12507, A
60	14.6	582	4	US-09-252-991A-13907	Sequence 12977, A
60	14.6	1449	4	US-09-252-991A-13298	Sequence 13298, A
60	14.6	2028	4	US-09-252-991A-12500	Sequence 12500, A
60	14.6	2040	4	US-09-252-991A-12977	Sequence 12977, A
59.5	14.5	1134	4	US-09-252-991A-8104	Sequence 8104, Ap
59.5	14.5	1314	4	US-09-252-991A-8001	Sequence 8001, Ap
59.5	14.5	1755	4	US-09-252-991A-8133	Sequence 8133, Ap
59.5	14.5	3003	3	US-08-915-337-1	Sequence 1, Appli
59	14.4	1450	4	US-09-354-998A-1	Sequence 1, Appli
59	14.4	1740	4	US-08-851-567B-50	Sequence 50, Appl
59	14.4	3913	1	US-08-472-934-7	Sequence 7, Appli
59	14.4	3913	2	US-08-323-460A-7	Sequence 7, Appli
59	14.4	3913	2	US-08-461-146C-7	Sequence 7, Appli
59	14.4	3913	3	US-08-461-146C-7	Sequence 7, Appli
59	14.4	3913	3	US-08-628-829-11	Sequence 11, Appl
59	14.4	4592	1	US-08-472-934-9	Sequence 9, Appli
59	14.4	4592	2	US-08-323-460A-9	Sequence 9, Appli
59	14.4	4592	2	US-08-461-146C-9	Sequence 9, Appli
59	14.4	4592	3	US-08-461-146C-9	Sequence 13, Appl
59	14.4	5414	4	US-08-628-829-13	

ALIGNMENTS

RESULT 1

US-09-023-655-79
; Sequence 79, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPLIB01
CLONE: 012364
US-09-023-655-79

Alignment Scores:	4.35e-50	Length:	786
Pred. No.:		Matches:	81
Score:	371.00	Conservative:	0
Percent Similarity:	96.43%	Mismatches:	0
Best Local Similarity:	96.43%	Indels:	3
Query Match:	90.49%	Gaps:	0
DB:	4		

US-09-648-310-4 (1-81) X US-09-023-655-79 (1-786)

Qy		MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys	20
Db		ATGAATGGGATCAGAGGTAAACCTTTAGTGAGGAAAATTCATCGTTGGGTTCAAAA	199
Qy		AsnAlaAspGlyLysLeuSer-ValLys-PheGlyValLeuPheArgAspAspLysCysA	40
Db		AATGCTGATGAAGAATTAAAGCGTGAATAATTTGGGTCCTCCGTGATGATAAATGTG	259
Qy		IaAsnLeuPheGluIaLeuValGlyThrLeuLysAlaIaLysArgArgLysIleVal	59
Db		CCAACCTCTTTGAAGCATGGTAGAACCTCTTAAGAGCTGC AAAACAAGGAGATTGTA	319
Qy		ThrTyProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeu	79
Db		ACATATCAGGAGAGCTGCTTCTCAAGGTTTCATGATGTTGACATTATATTACTG	379
Qy		GlnAsp	81
Db		CAAGAT	385

RESIST. 2

```

RESUL: 2
US-09-644-460-26
; Sequence 26, Application US/09644460
; Patent No. 6657053
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; TITLE OF INVENTION: Reciprocal Subtraction Differential
; FILE REFERENCE: Display
; CURRENT APPLICATION NUMBER: US/09/644,460
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US99/04323
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 09/197,889
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 09/185,115
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 09/032,684
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 800
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-644-460-26

```

```

Alignment Scores:
Pred. No.:      5.06e-47      Length:      800
Score:          352.00       Matches:      74

```

Percent Similarity:	93.98%	Conservative:	4
Best Local Similarity:	89.16%	Mismatches:	3
Query Match:	85.85%	Indels:	2
DB:	4	Gaps:	0

US-09-648-310-4 (1-81) x US-09-644-460-26 (1-800)

QY	1	MetAsnValAspHisGluValAsnLeuValGluGluLeuHisArgLeuGlySerLys	20
Db	170	ATGAACGGTGGAGCATGAGGTTAACTCTCGTGGAGAAATTCATCGTCTGGGTCCAAA	229
QY	21	AsnAlaAspGlyLysLeuSerValLysPheClyValLeuPheArgAspLysCysAla	40
Db	230	AATGCCGATGGAAACTGAGTGTGAGTTGGGTCTCTTCACAGCAGCATGTGCC	289
QY	41	AsnLeuPheGluAla-LeuValGlyThrLeuLysAla-AlaLysArgLysIleVal	60
Db	290	AATCTCTTTGAACCGTTGGTGGGAACCTCTGAAAGCCGCCAAACGAGAGATTGTTA	349
QY	60	hrTyrProGlyGluLeuLeuLeuClcGlyValHisAspAspValAspIleLeuLeuG	80
Db	350	CGTACGCAAGAGACTGCTTTTGCACAGTGTTATGATGATGATGATGATGCTGC	409
QY	80	InAsp	81
Db	410	AAGAT	414

RESULT, T 3

US-09-328-352-1774
; Sequence 1774, Application US/09328352
; Patent No. 6562958

```

1  GENERAL INFORMATION:
2  APPLICANT: Gary L. Breston et al.
3  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
4  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
5  FILE REFERENCE: GTC99-03PA
6  CURRENT APPLICATION NUMBER: US/09/328,352
7  CURRENT FILING DATE: 1999-06-04
8  NUMBER OF SEQ ID NOS: 8252
9  SEQ ID NO 1774
10 LENGTH: 2133

```

Alignment Scores:

Argument Scores:					
Pred. No.:	1.95	Length:	2133		
Score:	66.00	Matches:	24		
Percent Similarity:	50.67%	Conservative:	14		
Best Local Similarity:	32.00%	Mismatches:	29		
Query Match:	16.10%	Indels:	8		
DB:	4	Gaps:	4		

US-09-648-310-4 (1-81) X US-09-328-352-1774 (1-2133)

	OY	1	MetAsnValAspHisGluValAsnLeuLeuValGluGlutlleHisArgLeuGlyserLys	20
	Ddb	1396	ATGTGGTACCGCTGAACAACAACTGGTGCGTTATTGTCAT---TAGGAACGGGT	1452
			 ::: : :	:
	OY	21	Asn-----AlaspGlyIyIsLeuservalYlspheGlyValLeuPheArgAsp---	36
	Ddb	1453	AACCTACCATGCTATGAAGTCTGCATTTATACTGATTACGCCCTTAATGACCACCGATAAA	1512
			 ::: :	: : :
	OY	37	AsplyscysAlaAAsn-----LeuPheGluAlaLeuValGlyThrLeuLysAlaAla	53
	Ddb	1513	GACTTGTGTGAACACGTACACCGCTATTTCCAGAGCTCACGGGTATGGGTAAAAATGCCA	1572
			 : :	: : :
	OY	54	LysArgGlystleValThrTyrrProglygluleuLeuLeuGln	68
	Dd	1573	AAACTGAAAAGAATTACTCCTACGCATCACTTTACTCTGCATGCTCAG	1617
			::: : :	: : :

RESULT 4

US-09-252-991A-12137

```
; Sequence 12137, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12137
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12137

Alignment Scores:
Pred. No.: 0.293 Length: 393
Score: 64.50 Matches: 21
Percent Similarity: 39.51% Conservative: 11
Best Local Similarity: 25.93% Mismatches: 38
Query Match: 15.73% Indels: 11
Ds: 4 Gaps: 2

US-09-648-310-4 (1-81) x US-09-252-991A-12137 (1-393)

Qy 1 MetAsnValAspHisGluValAsnLeuLeuValGluHisArgLeuGlySerLys 20
Db 136 ATGAACGGCGACACACAAAGCACTCAACCCATCCGATCTCGTGAAGCGCTG-----AAA 189
Qy 21 AsnAlaAspGlyLysSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 190 CGCGCGGATGGTCACTCTTCGGCACGTCATAGCGGATGATCGAAGTGGCGAATCCGTCTC 249
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
Db 250 GACATCGCCCGCAGCTCGCGCGGTGGAAACGGCGGTACCGCGCAAGCGGCTCGT 309
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleLeuLeuGln 80
Db 310 -----ATCCACGACCATCATCGACCATTTGCTGCCCAT 342
Qy 81 Asp 81
Db 343 GAC 345

RESULT 5
US-08-358-901-1/c
; Sequence 1, Application US/08358901
; Patent No. 5554521
; GENERAL INFORMATION:
; APPLICANT: Suslow, Trevor V.
; APPLICANT: Jones, Jonathan D.G.
; TITLE OF INVENTION: No. 5554521el Chitinase-Producing Plants
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,901
```

```
; FILING DATE: 19-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/550,253
; FILING DATE: 09-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/889,033
; FILING DATE: 18-JUL-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/593,691
; FILING DATE: 26-MAR-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 12176-5-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 361..2043
US-08-358-901-1

Alignment Scores:
Pred. No.: 3.83 Length: 2323
Score: 64.50 Matches: 20
Percent Similarity: 52.94% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 31
Query Match: 15.73% Indels: 1
Db: 1 Gaps: 1

US-09-648-310-4 (1-81) x US-08-358-901-1 (1-2323)

Qy 5 HisGluValAsnLeuLeuValGluHisArgLeuGlySerLysAsnAlaAspGly 24
Db 1086 CACGCCCTTCGCGCCTTTTCAGCGCGCGACGGATCGTGGATCGAGATTTTGA-- 1030
Qy 25 LysLeuSerValLysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGlu 44
Db 1029 GTCTCGCGCCTTGGCAGGAGCGCTCAACGCTGGAAGTCCTTCAATCTCTTTTCAG 970
Qy 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGlu 64
Db 969 GCTGTGTTGATGCGATTGCGCGCGAGATCGGATAAGCCGTACAGCAGGTGGTTCAG 910
Qy 65 LeuLeuLeuGlnGlyValHisAsp 72
Db 909 GTTTTGGCGCGGATCTTGTGCAC 886

RESULT 6
US-08-566-347-1/c
; Sequence 1, Application US/08566347
; Patent No. 5633450
; GENERAL INFORMATION:
; APPLICANT: Suslow, Trevor V.
; APPLICANT: Jones, Jonathan D.G.
; TITLE OF INVENTION: No. 5633450el Chitinase-Producing Plants
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/566,347
FILING DATE: 01-DEC-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/358,901
FILING DATE: 19-DEC-1994
APPLICATION NUMBER: US 07/550,253
FILING DATE: 09-JUL-1990
APPLICATION NUMBER: US 06/888,033
FILING DATE: 18-JUL-1986
APPLICATION NUMBER: US 06/593,691
FILING DATE: 26-MAR-1984
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 12176-5-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2323 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 361..2043
US-08-566-347-1

Alignment Scores:
Pred. No.: 3.83 Length: 2323
Score: 64.50 Matches: 20
Percent Similarity: 52.94% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 31
Query Match: 15.73% Indels: 1
DB: 1 Gaps: 1

US-09-648-310-4 (1-81) x US-08-566-347-1 (1-2323)

QY 5 HisGluValAsnLeuValGluGluLeHisArgLeuGlySerLysAsnAlaAspGly 24
Db 1086 CAGCCCTTCTCGGCTTTTGACGCGCGGACGATCGTGATCGAGATTGAA--- 1030
QY 25 LysLeuSerValLysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGlu 44
Db 1029 GTCTCGGCGCTTGGCAGGCGCTGCAACGCTGGAAGCTGCTTCAATCTCTTCAG 970
QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGlu 64
Db 969 GCTGTGCTGTGATGCGATTCGCCCGCGACATCGGGATAAGCGGTACACAGGTGGTTCAG 910
QY 65 LeuLeuLeuGlnGlyValHisAsp 72
Db 909 GTTTTGGCGGGATCTTGTGCAC 886

RESULT 7

US-08-693-835-1/c
Sequence 1, Application US/08593835
Patent No. 5776448
GENERAL INFORMATION:
APPLICANT: Suslow, Trevor V.
APPLICANT: Jones, Jonathan D.G.
TITLE OF INVENTION: No. 5776448e1 Chitinase-Producing Plants

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,835
FILING DATE: 01-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/358,901
FILING DATE: 19-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/550,253
FILING DATE: 09-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/888,033
FILING DATE: 18-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/593,691
FILING DATE: 26-MAR-1984
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 12176-5-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2323 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 361..2043
US-08-693-835-1

Alignment Scores:
Pred. No.: 3.83 Length: 2323
Score: 64.50 Matches: 20
Percent Similarity: 52.94% Conservative: 16
Best Local Similarity: 29.41% Mismatches: 31
Query Match: 15.73% Indels: 1
DB: 1 Gaps: 1

US-09-648-310-4 (1-81) x US-08-693-835-1 (1-2323)

QY 5 HisGluValAsnLeuValGluGluLeHisArgLeuGlySerLysAsnAlaAspGly 24
Db 1086 CAGCCCTTCTCGGCTTTTGACGCGCGGACGATCGTGATCGAGATTGAA--- 1030
QY 25 LysLeuSerValLysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGlu 44
Db 1029 GTCTCGGCGCTTGGCAGGCGCTGCAACGCTGGAAGCTGCTTCAATCTCTTCAG 970
QY 45 AlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGlu 64
Db 969 GCTGTGCTGTGATGCGATTCGCCCGCGACATCGGGATAAGCGGTACACAGGTGGTTCAG 910
QY 65 LeuLeuLeuGlnGlyValHisAsp 72
Db 909 GTTTTGGCGGGATCTTGTGCAC 886

RESULT 8
US-08-457-797A-8/c
; Sequence 8, Application US/08457797A
; Patent No. 5869045
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,797A
; FILING DATE: June 1, 1995
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 18,839
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2329 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Serratia marcescens
; IMMEDIATE SOURCE:
; LIBRARY: Cosmid bank from Serratia marcescens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2329
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "exo-chitinase"
; OTHER INFORMATION: /product= "Chis protein"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /note= "sequence listing of the Chis gene from a
; OTHER INFORMATION: plasmid pLChis from E.coli A 5187"
US-08-457-797A-8
Alignment Scores:
Pred. No.: 4.63 Length: 2329
Score: 64.00 Matches: 17
Percent Similarity: 55.32% Conservative: 9
Best Local Similarity: 36.17% Mismatches: 21
Query Match: 15.61% Indels: 0
DB: 1 Gaps: 0
US-09-648-310-4 (1-81) x US-08-457-797A-8 (1-2329)
QY 26 LeuSerValIysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGluAla 45
Db 1026 CTCGCGCCCTGGCAGAGCGCTGCAACCGCTGGAGCTGCTTCAATCTCTTCAGGCT 967
QY 46 LeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGluLeu 65
Db 966 GTGCTTGGATCCATTGCGCGCAGATCGGATAAAGCGGTACAGCAGGTGGGTGAGTT 907
QY 66 LeuLeuGlnGlyValHisasp 72

Db 906 TTGCGCGGGATCTTGTGCAC 886
RESULT 9
US-08-812-025-8/c
; Sequence 8, Application US/08812025
; Patent No. 5804184
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,025
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teiser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2329 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Serratia marcescens
; IMMEDIATE SOURCE:
; LIBRARY: Cosmid bank from Serratia marcescens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2329
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "exo-chitinase"
; OTHER INFORMATION: /product= "Chis protein"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /note= "sequence listing of the Chis gene from a
; OTHER INFORMATION: plasmid pLChis from E.coli A 5187"
US-08-812-025-8
Alignment Scores:
Pred. No.: 4.63 Length: 2329
Score: 64.00 Matches: 17
Percent Similarity: 55.32% Conservative: 9
Best Local Similarity: 36.17% Mismatches: 21
Query Match: 15.61% Indels: 0
DB: 1 Gaps: 0
US-09-648-310-4 (1-81) x US-08-812-025-8 (1-2329)
QY 26 LeuSerValIysPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGluAla 45
Db 1026 CTCGCGCCCTGGCAGAGCGCTGCAACCGCTGGAGCTGCTTCAATCTCTTCAGGCT 967
QY 46 LeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGluLeu 65

Db 966 GTGCTGATCCATCCGCGCAGATCGGATGATAAAGCGGTACAGCAGGTGGTCAAGTT 907
 Qy 66 LeuLeuGlnGlyValHisasp 72
 Db 906 TTGCGCGGGATCTTGTGCAC 886

RESULT 10
 US-09-138-873A-8/c
 ; Sequence 8, Application US/09138873A
 ; Patent No. 6271438
 ; GENERAL INFORMATION:
 ; APPLICANT: Transgenic pathogen-resistant organism
 ; TITLE OF INVENTION: Transgenic pathogen-resistant organism
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Baker & Botts
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/138,873A
 ; FILING DATE: August 24, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tenser, Arthur
 ; REGISTRATION NUMBER: 18,839
 ; NAME: Kole, Lisa
 ; REGISTRATION NUMBER: 35,225
 ; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 408-2500
 ; TELEFAX: (212) 765-2519
 ; TELEX: 238555
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2329 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Serratia marcescens
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Cosmid bank from Serratia marcescens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1..2329
 ; IDENTIFICATION METHOD: experimental
 ; OTHER INFORMATION: /function= "exo-chitinase"
 ; OTHER INFORMATION: /product= "Chis protein"
 ; OTHER INFORMATION: /evidence= EXPERIMENTAL
 ; OTHER INFORMATION: /note= "sequence listing of the Chis gene from a
 ; OTHER INFORMATION: plasmid pLChis from E.coli A 5187"
 US-09-138-873A-8

Alignment Scores:
 Pred. No.: 4.63 Length: 2329
 Score: 64.00 Matches: 17
 Percent Similarity: 55.32% Conservative: 9
 Best Local Similarity: 36.17% Mismatches: 21
 Query Match: 15.61% Indels: 0
 DB: 3 Gaps: 0

US-09-648-310-4 (1-81) x US-09-138-873A-8 (1-2329)
 Qy 26 LeuSerValPheGlyValLeuPheArgAspLysCysAlaAsnLeuPheGluAla 45

Db 1026 CTCGCGGCTTGGCAGGCGCTGCAACGCTGCAAGCTCCCTTCAATCTCTTTCAAGCT 967
 Qy 46 LeuValGlyThrLeuLysAlaAlaLysArgGlyLysLeuValThrTyrProGlyGluLeu 65
 Db 966 GTCGTTGATGCCATTGCCCGCGCAGATCGGGATAAAGCCGTACAGCAGGTGGGTCAAGTT 907
 Qy 66 LeuLeuGlnGlyValHisasp 72
 Db 906 TTGCGCGGGATCTTGTGCAC 886

RESULT 11
 US-09-134-000C-2571
 ; Sequence 2571, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2571
 ; LENGTH: 1278
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-2571

Alignment Scores:
 Pred. No.: 2.81 Length: 1278
 Score: 63.00 Matches: 21
 Percent Similarity: 38.46% Conservative: 14
 Best Local Similarity: 23.08% Mismatches: 28
 Query Match: 15.37% Indels: 28
 DB: 4 Gaps: 2

US-09-648-310-4 (1-81) x US-09-134-000C-2571 (1-1278)
 Qy 1 MetAsnValAspHisGluValAsnLeuLeuValGluLeuHisArgLeuGlySerLys 20
 Db 55 ATGGACTTGGAAAAAGCTTTTAAACAAAGAACTGGAAGAGCTGTGCAGCAATTGGGAGTGAT 114
 Qy 21 AsnAlaAspGlyLysLeuSerVal----- 28
 Db 115 CTGCAGAGGAGGATGACAGCTTACTTTATACAGATTCTGTTGGTCAGCACAAGATAT 174
 Qy 29 -----LysPheGlyValLeuPheArgAspLysCysAlaAsnLeu 42
 Db 175 GTGCAAGGCAAACTGAGGCGTTTGGACTGGAAACGCAATTGACGAAGTCGGGATCTG 234
 Qy 43 PheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyLysLeuValThrTyrPro 62
 Db 235 TTTTGTGAGTGCAGGAACG-----GAATTTCCT 264
 Qy 63 GlyGluLeuLeuGlnGlyValHisasp 73
 Db 265 CAGGAACGATTTTACTGGGTCAATATCGAC 297

RESULT 12
 US-09-220-132-30
 ; Sequence 30, Application US/09220132
 ; Patent No. 6506607
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
 ; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 07334-074001
 ; CURRENT APPLICATION NUMBER: US/09/220,132
 ; CURRENT FILING DATE: 1998-12-23


```

RESULT 15
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Buit et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231580)..(231580)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g

```



```

; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664854)
; OTHER INFORMATION: n equals a, t, c, or g
;
US-08-916-421B-1

```

```

Alignment Scores:
Pred. No.: 1.26e+05 Length: 1664976
Score: 62.00 Matches: 23
Percent Similarity: 47.31% Conservative: 21
Best Local Similarity: 24.73% Mismatches: 29
Query Match: 15.12% Indels: 20
DB: 4 Gaps: 5

```

US-09-648-310-4 (1-81) x US-08-916-421B-1 (1-1664976)

```

QY 3 ValAspHisGluValAsn-----LeuLeuValGluGluIleHisArgLeuGlySer 19
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 720607 ATTGACATAGGTAGATGCCCTTTTGTTCAGAAATGCTAAATGCCGCTTGGT--- 720551

QY 20 LysAsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCys 39
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 720550 -----AGAAATGGCTTATTGCTGTAGGTATTGGAATCTGCTTAGAAGATGATGATGC 720497

QY 40 AlaAsnLeu-----PheGluAlaLeuValGlyThrLeuLys 51
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 720496 ATTAAGATAGGTAAATCAATCCTATGGGAGTATATAAAGAACTTATCAATGAATTTAA 720437

QY 52 AlaAlaLysArgArgLys-----IleValThrTyrProGlyGluLeuLeuGln 68
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 720436 AGTGTTAAACTAAATAAAATTAACAACATCTATTCTTTGAGGTAAGAAGGGGATGATT 720377

QY 69 GlyValHisAspValAspIleLeuLeuGlnAsp 81
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 720376 GGGATT-----ATTGCCTCTATATTGGTTGATGAT 720347

```

Search completed: September 1, 2004, 22:14:19
Job time : 238 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: September 1, 2004, 21:55:40 ; Search time 263.5 Seconds
(without alignments)
1512.848 Million cell updates/sec

Title: US-09-648-310-4
Perfect score: 410
Sequence: 1 MNVDHEVNLVEEIRHLSK.....PGEILLQGVHDDVILLQD 81

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3237270 seqs, 2460713050 residues
Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp
-Q=/cn2_1/USFTO_spool_p/US09648310/runat_27082004_154408_27994/app_query.fasta_1.526
-DB=Published Applications NA -QWTF=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCOR=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09648310 @CN 1.1 953 @runat_27082004_154408_27994
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:
4: /cn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
------------	-------	--------------------	----	-------------

1	410	100.0	400	13	US-10-085-783A-21733	Sequence 21733, A
2	410	100.0	400	16	US-10-242-535A-21733	Sequence 21733, A
3	410	100.0	483	13	US-10-085-783A-56189	Sequence 56189, A
4	410	100.0	483	16	US-10-242-535A-56189	Sequence 56189, A
5	410	100.0	627	12	US-09-969-034-557	Sequence 557, App
6	410	100.0	778	9	US-09-925-300-545	Sequence 545, App
7	410	100.0	835	13	US-10-373-556-3	Sequence 3, Appli
8	410	100.0	835	13	US-10-373-556-6	Sequence 6, Appli
9	410	100.0	876	13	US-10-342-887-156	Sequence 156, App
10	410	100.0	876	13	US-10-172-118-156	Sequence 156, App
11	406	99.0	594	12	US-09-969-034-750	Sequence 750, App
12	404	98.5	717	12	US-09-969-034-748	Sequence 748, App
13	390	95.1	780	13	US-10-373-556-1	Sequence 1, Appli
14	390	95.1	780	13	US-10-373-556-5	Sequence 5, Appli
15	387	94.4	488	10	US-09-918-993-26075	Sequence 26075, A
16	377	90.5	786	17	US-10-641-643-79	Sequence 79, Appl
17	352	85.9	800	17	US-10-725-969A-26	Sequence 26, Appl
18	295	72.0	533	13	US-10-425-114-19867	Sequence 19867, A
19	286	69.8	486	9	US-09-938-842A-355	Sequence 355, App
20	286	69.8	486	11	US-09-938-842A-355	Sequence 355, App
21	286	69.8	492	10	US-09-770-961-618	Sequence 618, App
22	276	67.3	818	17	US-10-437-963-43648	Sequence 43648, A
23	269	65.6	716	13	US-10-424-599-94878	Sequence 94878, A
24	252	61.5	552	9	US-09-920-300A-939	Sequence 939, App
25	252	61.5	552	14	US-10-033-528-939	Sequence 939, App
26	252	61.5	552	15	US-10-099-926-939	Sequence 939, App
27	231	56.3	268	9	US-09-294-093B-2020	Sequence 2020, Ap
28	216	52.7	388	9	US-09-925-299-318	Sequence 318, App
29	216	52.7	388	10	US-09-925-299-318	Sequence 318, App
30	149	36.3	289	9	US-09-294-093B-4150	Sequence 4150, Ap
31	108	26.3	388	16	US-10-191-803-820	Sequence 820, App
32	105	25.6	60	10	US-09-908-975-22102	Sequence 22102, A
33	104	25.4	1128	17	US-10-644-659A-3	Sequence 3, Appli
34	102	24.9	1146	17	US-10-644-659A-1	Sequence 1, Appli
35	102	24.9	1322	16	US-10-104-047-1199	Sequence 1199, Ap
36	94.5	23.0	489	17	US-10-644-659A-7	Sequence 7, Appli
37	86	21.0	175	9	US-09-294-093B-5438	Sequence 5438, Ap
38	80.5	19.6	2960	17	US-10-437-963-34365	Sequence 34365, A
39	72.5	17.7	1359	17	US-10-437-963-82252	Sequence 82252, A
40	71.5	17.4	1107	13	US-10-425-114-33943	Sequence 33943, A
41	71.5	17.4	2163	13	US-10-425-114-30828	Sequence 30828, A
42	70	17.1	1728	13	US-10-282-122A-16022	Sequence 16022, A
43	68	16.6	2232	17	US-10-437-963-53833	Sequence 53833, A
44	67	16.3	2062	13	US-10-424-599-142059	Sequence 142059, A
45	66	16.1	553	17	US-10-437-963-92788	Sequence 92788, A

ALIGNMENTS

RESULT 1
US-10-085-783A-21733
; Sequence 21733, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Lieuw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10085783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21733
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human


```
US-09-648-310-4 (1-81) x US-10-085-783A-56189 (1-483)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 81 ATGAATGTGGATCAGGAGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTTCAAAA 140
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 141 AATGCTGATGGAAGTTAGCTGAATTTGGGGTCTCTCCGGAAGTAATGTC 200
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyIleValThr 60
Db 201 AACCTCTTTGAAGCATGCTAGCAACTCTTAAAGCTGCAAAACGAAGATGTAACA 260
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleLeuLeuGln 80
Db 261 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCAATGATGTTGACATTATATTACTGCAA 320
QY 81 Asp 81
Db 321 GAT 323
RESULT 4
US-10-242-535A-56189
; Sequence 56189, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56189
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-56189
Alignment Scores:
Pred. No.: 2,59e-58 Length: 483
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-09-648-310-4 (1-81) x US-10-242-535A-56189 (1-483)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 81 ATGAATGTGGATCAGGAGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTTCAAAA 140
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 141 AATGCTGATGGAAGTTAGCTGAATTTGGGGTCTCTCCGGAAGTAATGTC 200
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyIleValThr 60
Db 201 AACCTCTTTGAAGCATGCTAGCAACTCTTAAAGCTGCAAAACGAAGATGTAACA 260
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleLeuLeuGln 80
Db 261 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCAATGATGTTGACATTATATTACTGCAA 320
QY 81 Asp 81
Db 321 GAT 323
RESULT 5
US-09-969-034-557/c
; Sequence 557, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 557
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 503..512, 539, 596, 620
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-557
Alignment Scores:
Pred. No.: 3.82e-58 Length: 627
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-648-310-4 (1-81) x US-09-969-034-557 (1-627)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 271 ATGAATGTGGATCAGGAGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTTCAAAA 212
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 211 AATGCTGATGGAAGTTAAAGCGTGAATTTGGGGTCTCTTCCTGATGATAAATGTGCC 152
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgGlyIleValThr 60
Db 151 AACCTCTTTGAAGCATGCTAGCAACTCTTAAAGCTGCAAAACGAAGATGTAACA 92
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleLeuLeuGln 80
Db 91 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCAATGATGTTGACATTATATTACTGCAA 320
QY 81 Asp 81
Db 31 GAT 29
RESULT 6
US-09-925-300-545
; Sequence 545, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
```

; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: FA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 545
 ; LENGTH: 778
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (641)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (652)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-925-300-545

Alignment Scores:
 Pred. No.: 5,28e-58 Length: 778
 Score: 410.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-648-310-4 (1-81) x US-09-925-300-545 (1-778)

QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20
 Db 186 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGAAATTCATCGTTGGTTCAAAA 245
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
 Db 246 AATGCTGTAGTGAAGTAAAGCTGAAATTTGGGGTCTCTCCGTGATGATAAATGTGCC 305
 QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
 Db 306 AACCTCTTTGAAGCATGTGTAGAACTCTTAAGCTGCAAAACGAAGGAAGATTGTAA 365
 QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
 Db 366 TATCCAGGAGAGTGTCTTCTGCAAGGTGTTCATGATGATGATGATATATTACTGCA 425
 QY 81 Asp 81
 Db 426 GAT 428

RESULT 7
 US-10-373-556-3
 ; Sequence 3, Application US/10373556
 ; Publication No. US20030224402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul B. Fisher
 ; APPLICANT: Dong-chul Kang
 ; APPLICANT: Zao-Zhong Su
 ; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
 ; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
 ; CURRENT FILING DATE: 2003-02-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/26795
 ; PRIOR FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: 09/648,310
 ; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 835
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-373-556-3

Alignment Scores:
 Pred. No.: 5,86e-58 Length: 835
 Score: 410.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-648-310-4 (1-81) x US-10-373-556-3 (1-835)

QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20
 Db 197 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGAAATTCATCGTTGGTTCAAAA 256
 QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
 Db 257 AATGCTGTAGTGAAGTAAAGCTGAAATTTGGGGTCTCTCCGTGATGATAAATGTGCC 316
 QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
 Db 317 AACCTCTTTGAAGCATGTGTAGAACTCTTAAGCTGCAAAACGAAGGAAGATTGTAA 376
 QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
 Db 377 TATCCAGGAGAGTGTCTTCTGCAAGGTGTTCATGATGATGATGATATATTACTGCA 436
 QY 81 Asp 81
 Db 437 GAT 439

RESULT 8
 US-10-373-556-6
 ; Sequence 6, Application US/10373556
 ; Publication No. US20030224402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul B. Fisher
 ; APPLICANT: Dong-chul Kang
 ; APPLICANT: Zao-Zhong Su
 ; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
 ; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
 ; CURRENT FILING DATE: 2003-02-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/26795
 ; PRIOR FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: 09/648,310
 ; PRIOR FILING DATE: 2000-08-25
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 835
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-373-556-6

Alignment Scores:
 Pred. No.: 5,86e-58 Length: 835
 Score: 410.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-648-310-4 (1-81) x US-10-373-556-6 (1-835)

QY 1 MetAsnValAspHisGluValAsnLeuValGluLeuHisArgLeuGlySerLys 20

```

Db 197 ATGAATGGGATCAGAGGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTCAAAA 256
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 257 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTTCCTGATGATAAATGTGCC 316
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaLysArgLysIleValThr 60
Db 317 AACCTCTTTGAAGCATTTGGTAGGAACCTTAAAGCTGCAAAACGAAGAGATTGTAACA 376
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
Db 377 TATCCAGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATTATATTACTGCAA 436
Qy 81 Asp 81
Db 437 GAT 439

```

RESULT 9

```

US-10-342-887-156
; Sequence 156, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 156
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF116682
; DATABASE ENTRY DATE: 2001-06-18
US-10-342-887-156

```

Alignment Scores:

```

Pred. No.: 6,3e-58 Length: 876
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-648-310-4 (1-81) x US-10-342-887-156 (1-876)
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-156

```

Alignment Scores:

```

Pred. No.: 6,3e-58 Length: 876
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

```

US-09-648-310-4 (1-81) x US-10-342-887-156 (1-876)

```

```

Qy 1 MetAsnValAspHisGluValAsnLeuValGluIleHisArgLeuGlySerLys 20
Db 136 ATGAATGGGATCAGAGGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTCAAAA 195
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 196 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTTCCTGATGATAAATGTGCC 255
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaLysArgLysIleValThr 60
Db 256 AACCTCTTTGAAGCATTTGGTAGGAACCTTAAAGCTGCAAAACGAAGAGATTGTAACA 315
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80

```

```

Db 316 TATCCAGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATTATATTACTGCAA 375
Qy 81 Asp 81
Db 376 GAT 378

```

RESULT 10

```

US-10-172-118-156
; Sequence 156, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 156
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF116682
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-156

```

Alignment Scores:

```

Pred. No.: 6,3e-58 Length: 876
Score: 410.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

```

US-09-648-310-4 (1-81) x US-10-172-118-156 (1-876)

```

```

Qy 1 MetAsnValAspHisGluValAsnLeuValGluIleHisArgLeuGlySerLys 20
Db 136 ATGAATGGGATCAGAGGTTAACTCTTAGTGAGGAAATTCATCGTTGGGTCAAAA 195
Qy 21 AsnAlaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 196 AATGCTGATGGAAGTTAAGCGTGAATTTGGGGTCTCTTCCTGATGATAAATGTGCC 255
Qy 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaLysArgLysIleValThr 60
Db 256 AACCTCTTTGAAGCATTTGGTAGGAACCTTAAAGCTGCAAAACGAAGAGATTGTAACA 315
Qy 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspIleLeuLeuGln 80
Db 316 TATCCAGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATTATATTACTGCAA 375
Qy 81 Asp 81
Db 376 GAT 378

```

RESULT 11

```

US-09-969-034-750
; Sequence 750, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III

```

; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 750
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 405, 447, 472, 485, 497, 513, 534, 537, 541, 543, 563, 572
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-750

Alignment Scores:
Pred. No.: 1,64e-57 Length: 594
Score: 406.00 Matches: 80
Percent Similarity: 100.00%
Best Local Similarity: 98.77%
Query Match: 99.02%
Indels: 0
DB: 12
Gaps: 0

US-09-648-310-4 (1-81) x US-09-969-034-750 (1-594)

QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 199 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGGAAATTCATCGTTGGGTTCAAAA 258
QY 21 AsnAlaAspGlyValSerValLysPheGlyValLeuPheArgAspLysCysAla 40
Db 259 AATGCTGTAGTGAAGAGTTAAGCGTGAATTTGGGGTCTCTCCGTGATGATAATGTGCC 318
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysValThr 60
Db 319 AACCTCTTTGAAGCATTTGTAGGAACCTTTAAAGCTGCAAAAGGAAGATTGTAACA 378
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspLysLeuLeuGln 80
Db 379 TATCCAGGAGAGCTGCTTCTACAGGNGTTTCATGATGATTTGACATTATATTACTGCAA 438
QY 81 Asp 81
Db 439 GAA 441

RESULT 12

US-09-969-034-748
; Sequence 748, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271

; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 452, 481, 482, 505, 521, 536, 540, 594, 599, 607, 635, 641,
; LOCATION: 643, 657, 664, 673, 691, 695, 700
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-748

Alignment Scores:
Pred. No.: 4,68e-57 Length: 717
Score: 404.00 Matches: 80
Percent Similarity: 100.00%
Best Local Similarity: 98.54%
Query Match: 98.54%
Indels: 0
DB: 12
Gaps: 0

US-09-648-310-4 (1-81) x US-09-969-034-748 (1-717)

QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 202 ATGAATGTGGATCAGGAGTTAACTCTTAGTGGAGGAAATTCATCGTTGGGTTCAAAA 261
QY 21 AsnAlaAspGlyValSerValLysPheGlyValLeuPheArgAspLysCysAla 40
Db 262 AATGCTGTAGTGAAGAGTTAAGCGTGAATTTGGGGTCTCTCCGTGATGATAATGTGCC 321
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysValThr 60
Db 322 AACCTCTTTGAAGCATTTGTAGGAACCTTTAAAGCTGCAAAAGGAAGATTGTAACA 381
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspLysLeuLeuGln 80
Db 382 TATCCAGGAGAGCTGCTTCTACAGGTTTCATGATGATTTGACATTATATTACTGCAA 441

RESULT 13

US-10-373-556-1
; Sequence 1, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zhao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050.2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 780
; TYPE: DNA
; ORGANISM: rattus norvegicus
US-10-373-556-1
Alignment Scores:
Pred. No.: 1,15e-54 Length: 780
Score: 390.00 Matches: 76
Percent Similarity: 98.77%
Best Local Similarity: 93.83%
Query Match: 95.12%
Indels: 0
DB: 13
Gaps: 0


```
US-09-648-310-4 (1-81) x US-10-373-556-1 (1-780)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 170 ATGAACGTGGACATGAGGTTAACTCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAA 229
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 230 AATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCTCTTCCAAAGACGACAGATGTGCC 289
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
Db 290 AATCTCTTTGAACGTTGGTGGAACTCTGAAGCGCGAAACGAGGAAGATTGTTACG 349
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspLysIleLeuGln 80
Db 350 TACGCAGGAGAGTGCTTTTGAAGGTGTTTCATGATGATGTTGACATTGTTGCTGCAA 409
QY 81 Asp 81
Db 410 GAT 412
RESULT 14
US-10-373-556-5
; Sequence 5, Application US/10373556
; Publication No. US20030224402A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher
; APPLICANT: Dong-chul Kang
; APPLICANT: Zao-Zhong Su
; TITLE OF INVENTION: PROGRESSION SUPPRESSED GENE 13 (PSGen13)
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: A34586-A-PCT-USA (070050,2305)
; CURRENT APPLICATION NUMBER: US/10/373,556
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: PCT/US01/26795
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/648,310
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: rattus norvegicus
US-10-373-556-5
Alignment Scores:
Pred. No.: 1.15e-54 Length: 780
Score: 390.00 Matches: 76
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 93.83% Mismatches: 1
Query Match: 95.12% Indels: 0
DB: 13 Gaps: 0
US-09-648-310-4 (1-81) x US-10-373-556-5 (1-780)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 170 ATGAACGTGGACATGAGGTTAACTCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAA 229
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 230 AATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCTCTTCCAAAGACGACAGATGTGCC 289
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
Db 290 AATCTCTTTGAACGTTGGTGGAACTCTGAAGCGCGAAACGAGGAAGATTGTTACG 349
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspLysIleLeuGln 80
Db 350 TACGCAGGAGAGTGCTTTTGAAGGTGTTTCATGATGATGTTGACATTGTTGCTGCAA 409
US-09-648-310-4 (1-81) x US-09-918-995-26075 (1-458)
QY 1 MetAsnValAspHisGluValAsnLeuValGluGluHisArgLeuGlySerLys 20
Db 231 ATGATCTGGATCAGGAGTTAACTCTTAGTGAGGAAATTCATCGTCTGGGTTCAAAA 290
QY 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
Db 291 AATGCTGATGAAAGTTAAGCGTGAATTTGGGGTCTCTCTCCGTGATGATAAATGTGCC 350
QY 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgLysIleValThr 60
Db 351 AACCTCTTTGAAGCATTTGTTAGGAACTCTTAAAGCTGCAAAACGAGGAAGATTGTAACA 410
QY 61 TyrProGlyGluLeuLeuGlnGlyValHisAspValAspLysIleLeuGln 76
Db 411 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTTCATGATGATGTTGACATT 458
Search completed: September 2, 2004, 00:02:01
Job time : 265.5 secs
```

This Page Blank (uspto)